OIPE

RAW SEQUENCE LISTING   DATE: 05/22/2003
PATENT APPLICATION: **US/10/055,624B**   TIME: 11:27:49

Input Set : **A:\sequence listing 10-055,624 created 05-07-2003.txt**
Output Set: **N:\CRF4\05222003\J055624B.raw**

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 3 <110> APPLICANT: Adams, Sean H
 4        Chui, Clarissa
 5        Goddard, Audrey D
 6        Grimaldi, J. Christopher
 8 <120> TITLE OF INVENTION: BFIT COMPOSITIONS AND METHODS OF USE
10 <130> FILE REFERENCE: 9800081-0066
12 <140> CURRENT APPLICATION NUMBER: 10/055,624B
13 <141> CURRENT FILING DATE: 2002-01-22
15 <150> PRIOR APPLICATION NUMBER: US 60/263,362
16 <151> PRIOR FILING DATE: 2002-01-22
18 <160> NUMBER OF SEQ ID NOS: 23
20 <170> SOFTWARE: PatentIn version 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1857
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
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32 atggcagacg gcgagggata ccggaacccc acggaggtgc agatgagcca gctggtgctg    180
34 ccctgccaca ccaaccaacg tggtgagctg agcgtcgggc agctgctcaa gtggattgac    240
36 accacggctt gcctgtccgc ggagaggcac gctggctgcc cctgtgtcac agcttccatg    300
38 gatgacatct attttgagca caccattagt gttggacaag tggtgaatat caaggccaag    360
40 gtgaaccggg ccttcaactc cagcatggag gtgggcatcc aggtggcctc ggaggacctg    420
42 tgctctgaga agcagtggaa tgtgtgcaag gccttggcca ccttcgtggc cgccgagag     480
44 atcaccaagg tgaagctgaa gcagatcacg ccgcggacag aagaggagaa gatggagcac    540
46 agtgtggcgg ctgagcgccg gcgcatgcgc cttgtctatg cagacaccat caaggacctc    600
48 ctggccaact gcgccattca gggcgatctg gagagcagag actgtagccg catggtgccg    660
50 gctgagaaga cccgtgtgga gagtgtggag ctggtcctgc ctccccacgc caatcaccag    720
52 ggcaacacct ttggggggcca gatcatggcc tggatggaga atgtggccac cattgcagcc    780
54 agccggctct gccgtgccca ccctacgctg aaggccattg aaatgttcca cttccgaggc    840
56 ccgtcccagg tcggcgaccg tctggtgctc aaagccatcg tgaacaatgc cttcaaacat    900
58 agcatggagg tgggcgtgtg cgtggaggcc tatcgccagg aggctgagac ccaccggcgc    960
60 cacatcaaca gtgcctttat gacctttgtg gtcctggacg cagatgacca gccccagttg   1020
62 ctgccctgga ttcggcccca gcccggcgat ggtgagcggc ggtaccgaga ggccagtgcc   1080
64 agaaagaaga tccgcctgga caggaagtac atcgtgtcct gtaagcagac agaggtgccc   1140
66 ctctccgtcc cctgggaccc tagcaaccag gtgtacctga gctacaataa cgtctcctcc   1200
68 ttgaagatgc ttgtggccaa ggacaactgg gtgctgtcct cggagatcag tcaggtccgc   1260
70 ctgtacactc tggaggatga caagttcctc tccttccaca tggagatggt ggtgcatgtg   1320
72 gatgcagccc aggccttcct gctgctctcg gacctgcgtc agaggccaga gtgggacaag   1380
74 cactaccgga gcgtggagct agtgcagcag gtagacgagg acgacgccat ctaccacgtc   1440
76 accagccctg ccctcggagg tcacacaaag ccccaggact tcgtgatcct ggcctcgagg   1500
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80 acacaccgag agacgccaga gtacagacgc ggagagaccc tctgctcagg cttctgcctc  1620
82 tggcgcgagg gggaccagct gaccaagtgc tgctgggtta gggtctccct gactgagctg  1680
84 gtctcggcaa gtggcttcta ttcctggggg ctcgaatcca ggtcaaaggg tcgcaggagc  1740
86 gacggttgga atggaaaact agctggagga cacctgagta ctcttaaagc aatccccgtg  1800
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103             20                  25                  30
106 Ser Ala Met Ala Asp Gly Glu Gly Tyr Arg Asn Pro Thr Glu Val Gln
107             35                  40                  45
110 Met Ser Gln Leu Val Leu Pro Cys His Thr Asn Gln Arg Gly Glu Leu
111     50                  55                  60
114 Ser Val Gly Gln Leu Leu Lys Trp Ile Asp Thr Thr Ala Cys Leu Ser
115 65                  70                  75                  80
118 Ala Glu Arg His Ala Gly Cys Pro Cys Val Thr Ala Ser Met Asp Asp
119             85                  90                  95
122 Ile Tyr Phe Glu His Thr Ile Ser Val Gly Gln Val Val Asn Ile Lys
123             100                 105                 110
126 Ala Lys Val Asn Arg Ala Phe Asn Ser Ser Met Glu Val Gly Ile Gln
127         115                 120                 125
130 Val Ala Ser Glu Asp Leu Cys Ser Glu Lys Gln Trp Asn Val Cys Lys
131     130                 135                 140
134 Ala Leu Ala Thr Phe Val Ala Arg Arg Glu Ile Thr Lys Val Lys Leu
135 145                 150                 155                 160
138 Lys Gln Ile Thr Pro Arg Thr Glu Glu Glu Lys Met Glu His Ser Val
139             165                 170                 175
142 Ala Ala Glu Arg Arg Arg Met Arg Leu Val Tyr Ala Asp Thr Ile Lys
143             180                 185                 190
146 Asp Leu Leu Ala Asn Cys Ala Ile Gln Gly Asp Leu Glu Ser Arg Asp
147         195                 200                 205
150 Cys Ser Arg Met Val Pro Ala Glu Lys Thr Arg Val Glu Ser Val Glu
151     210                 215                 220
154 Leu Val Leu Pro Pro His Ala Asn His Gln Gly Asn Thr Phe Gly Gly
155 225                 230                 235                 240
158 Gln Ile Met Ala Trp Met Glu Asn Val Ala Thr Ile Ala Ala Ser Arg
159             245                 250                 255
162 Leu Cys Arg Ala His Pro Thr Leu Lys Ala Ile Glu Met Phe His Phe
163         260                 265                 270
166 Arg Gly Pro Ser Gln Val Gly Asp Arg Leu Val Leu Lys Ala Ile Val
167         275                 280                 285
170 Asn Asn Ala Phe Lys His Ser Met Glu Val Gly Val Cys Val Glu Ala
171     290                 295                 300
174 Tyr Arg Gln Glu Ala Glu Thr His Arg Arg His Ile Asn Ser Ala Phe
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183            340                 345                 350
186 Ser Ala Arg Lys Lys Ile Arg Leu Asp Arg Lys Tyr Ile Val Ser Cys
187            355                 360                 365
190 Lys Gln Thr Glu Val Pro Leu Ser Val Pro Trp Asp Pro Ser Asn Gln
191        370                 375                 380
194 Val Tyr Leu Ser Tyr Asn Asn Val Ser Ser Leu Lys Met Leu Val Ala
195 385                 390                 395                 400
198 Lys Asp Asn Trp Val Leu Ser Ser Glu Ile Ser Gln Val Arg Leu Tyr
199                405                 410                 415
202 Thr Leu Glu Asp Asp Lys Phe Leu Ser Phe His Met Glu Met Val Val
203            420                 425                 430
206 His Val Asp Ala Ala Gln Ala Phe Leu Leu Leu Ser Asp Leu Arg Gln
207            435                 440                 445
210 Arg Pro Glu Trp Asp Lys His Tyr Arg Ser Val Glu Leu Val Gln Gln
211        450                 455                 460
214 Val Asp Glu Asp Asp Ala Ile Tyr His Val Thr Ser Pro Ala Leu Gly
215 465                 470                 475                 480
218 Gly His Thr Lys Pro Gln Asp Phe Val Ile Leu Ala Ser Arg Arg Lys
219            485                 490                 495
222 Pro Cys Asp Asn Gly Asp Pro Tyr Val Ile Ala Leu Arg Ser Val Thr
223            500                 505                 510
226 Leu Pro Thr His Arg Glu Thr Pro Glu Tyr Arg Arg Gly Glu Thr Leu
227            515                 520                 525
230 Cys Ser Gly Phe Cys Leu Trp Arg Glu Gly Asp Gln Leu Thr Lys Cys
231        530                 535                 540
234 Cys Trp Val Arg Val Ser Leu Thr Glu Leu Val Ser Ala Ser Gly Phe
235 545                 550                 555                 560
238 Tyr Ser Trp Gly Leu Glu Ser Arg Ser Lys Gly Arg Arg Ser Asp Gly
239            565                 570                 575
242 Trp Asn Gly Lys Leu Ala Gly Gly His Leu Ser Thr Leu Lys Ala Ile
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251 <211> LENGTH: 1818
252 <212> TYPE: DNA
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260 tgccatggca gacggcgagg gataccggaa ccccacggag gtgcagatga gccagctggt     180
262 gctgccctgc cacaccaacc aacgtggtga gctgagcgtc gggcagctgc tcaagtggat     240
264 tgacaccacg gcttgcctgt ccgcggagag gcacgctggc tgcccctgtg tcacagcttc     300
266 catggatgac atctatttg agcacaccat tagtgttgga caagtggtga atatcaaggc     360
268 caaggtgaac cgggccttca actccagcat ggaggtgggc atccaggtgg cctcggagga     420
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270 cctgtgctct gagaagcagt ggaatgtgtg caaggccttg gccaccttcg tggcccgccg    480
272 agagatcacc aaggtgaagc tgaagcagat cacgccgcgg acagaagagg agaagatgga    540
274 gcacagtgtg gcggctgagc gccggcgcat gcgccttgtc tatgcagaca ccatcaagga    600
276 cctcctggcc aactgcgcca ttcagggcga tctggagagc agagactgta gccgcatggt    660
278 gccggctgag aagacccgtg tggagagtgt ggagctggtc ctgcctcccc acgccaatca    720
280 ccagggcaac acctttgggg gccagatcat ggcctggatg gagaatgtgg ccaccattgc    780
282 agccagccgg ctctgccgtg cccaccctac gctgaaggcc attgaaatgt tccacttccg    840
284 aggcccgtcc caggtcggcg accgtctggt gctcaaagcc atcgtgaaca atgccttcaa    900
286 acatagcatg gaggtgggcg tgtgcgtgga ggcctatcgc caggaggctg agacccaccg    960
288 gcgccacatc aacagtgcct ttatgacctt tgtggtcctg gacgcagatg accagcccca   1020
290 gttgctgccc tggattcggc cccagcccgg cgatggtgag cggcggtacc gagaggccag   1080
292 tgccagaaag aagatccgcc tggacaggaa gtacatcgtg tcctgtaagc agacagaggt   1140
294 gcccctctcc gtcccctggg accctagcaa ccaggtgtac ctgagctaca ataacgtctc   1200
296 ctccttgaag atgcttgtgg ccaaggacaa ctgggtgctg tcctcggaga tcagtcaggt   1260
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312 tgttctcaac tatgtgacca ccaacgtggc cggcctctcc tctgagttct acaccacctt   1740
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321 <212> TYPE: PRT
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331             20                  25                  30
334 Ser Ala Met Ala Asp Gly Glu Gly Tyr Arg Asn Pro Thr Glu Val Gln
335         35                  40                  45
338 Met Ser Gln Leu Val Leu Pro Cys His Thr Asn Gln Arg Gly Glu Leu
339     50                  55                  60
342 Ser Val Gly Gln Leu Leu Lys Trp Ile Asp Thr Thr Ala Cys Leu Ser
343 65                  70                  75                  80
346 Ala Glu Arg His Ala Gly Cys Pro Cys Val Thr Ala Ser Met Asp Asp
347             85                  90                  95
350 Ile Tyr Phe Glu His Thr Ile Ser Val Gly Gln Val Val Asn Ile Lys
351             100                 105                 110
354 Ala Lys Val Asn Arg Ala Phe Asn Ser Ser Met Glu Val Gly Ile Gln
355         115                 120                 125
358 Val Ala Ser Glu Asp Leu Cys Ser Glu Lys Gln Trp Asn Val Cys Lys
359     130                 135                 140
362 Ala Leu Ala Thr Phe Val Ala Arg Arg Glu Ile Thr Lys Val Lys Leu
363 145                 150                 155                 160
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366 Lys Gln Ile Thr Pro Arg Thr Glu Glu Lys Met Glu His Ser Val
367             165             170             175
370 Ala Ala Glu Arg Arg Arg Met Arg Leu Val Tyr Ala Asp Thr Ile Lys
371             180             185             190
374 Asp Leu Leu Ala Asn Cys Ala Ile Gln Gly Asp Leu Glu Ser Arg Asp
375         195             200             205
378 Cys Ser Arg Met Val Pro Ala Glu Lys Thr Arg Val Glu Ser Val Glu
379     210             215             220
382 Leu Val Leu Pro Pro His Ala Asn His Gln Gly Asn Thr Phe Gly Gly
383 225             230             235             240
386 Gln Ile Met Ala Trp Met Glu Asn Val Ala Thr Ile Ala Ala Ser Arg
387             245             250             255
390 Leu Cys Arg Ala His Pro Thr Leu Lys Ala Ile Glu Met Phe His Phe
391             260             265             270
394 Arg Gly Pro Ser Gln Val Gly Asp Arg Leu Val Leu Lys Ala Ile Val
395             275             280             285
398 Asn Asn Ala Phe Lys His Ser Met Glu Val Gly Val Cys Val Glu Ala
399     290             295             300
402 Tyr Arg Gln Glu Ala Glu Thr His Arg Arg His Ile Asn Ser Ala Phe
403 305             310             315             320
406 Met Thr Phe Val Val Leu Asp Ala Asp Asp Gln Pro Gln Leu Leu Pro
407             325             330             335
410 Trp Ile Arg Pro Gln Pro Gly Asp Gly Glu Arg Arg Tyr Arg Glu Ala
411             340             345             350
414 Ser Ala Arg Lys Lys Ile Arg Leu Asp Arg Lys Tyr Ile Val Ser Cys
415         355             360             365
418 Lys Gln Thr Glu Val Pro Leu Ser Val Pro Trp Asp Pro Ser Asn Gln
419     370             375             380
422 Val Tyr Leu Ser Tyr Asn Asn Val Ser Ser Leu Lys Met Leu Val Ala
423 385             390             395             400
426 Lys Asp Asn Trp Val Leu Ser Ser Glu Ile Ser Gln Val Arg Leu Tyr
427             405             410             415
430 Thr Leu Glu Asp Asp Lys Phe Leu Ser Phe His Met Glu Met Val Val
431             420             425             430
434 His Val Asp Ala Ala Gln Ala Phe Leu Leu Leu Ser Asp Leu Arg Gln
435         435             440             445
438 Arg Pro Glu Trp Asp Lys His Tyr Arg Ser Val Glu Leu Val Gln Gln
439     450             455             460
442 Val Asp Glu Asp Asp Ala Ile Tyr His Val Thr Ser Pro Ala Leu Gly
443 465             470             475             480
446 Gly His Thr Lys Pro Gln Asp Phe Val Ile Leu Ala Ser Arg Arg Lys
447             485             490             495
450 Pro Cys Asp Asn Gly Asp Pro Tyr Val Ile Ala Leu Arg Ser Val Thr
451             500             505             510
454 Leu Pro Thr His Arg Glu Thr Pro Glu Tyr Arg Arg Gly Glu Thr Leu
455         515             520             525
458 Cys Ser Gly Phe Cys Leu Trp Arg Glu Gly Asp Gln Leu Thr Lys Val
459     530             535             540
462 Ser Tyr Tyr Asn Gln Ala Thr Pro Gly Val Leu Asn Tyr Val Thr Thr
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VERIFICATION SUMMARY   DATE: 05/22/2003
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